FIG. 1

FS-HBP1

```
T3→
1   AGAAAGCCAACATGAAGCTTCTGCTCTCTCTTGCCTTCGTCTTAGCTCTCAGCCAAGTTA   60
              M  K  L  L  L  S  L  A  F  V  L  A  L  S  Q  V  K

61  AAGCCGATAAGCCAGTTTGGGCGGATGAAGCGGCAAACGGGGAACACCAAGACGCCTGGA  120
      A  D  K  P  V  W  A  D  E  A  A  N  G  E  H  Q  D  A  W  K
         ↑

121 AGCATCTCCAAAAACTCGTTGAAGAGAATTACGACTTGATAAAAGCCACCTACAAGAACG  180
      H  L  Q  K  L  V  E  E  N  Y  D  L  I  K  A  T  Y  K  N  D

                                          T3a→  ←T7c
181 ACCCAGTTTGGGGTAACGACTTCACTTGCGTGGGTACTGCAGCGCAGAATTTGAACGAGG  240
      P  V  W  G  N  D  F  T  C  V  G  T  A  A  Q  N  L  N  E  D

241 ACGAGAAGAACGTTGAAGCATGGTTTATGTTTATGAATAATGCTGATACCGTATACCAAC  300
      E  K  N  V  E  A  W  F  M  F  M  N  N  A  D  T  V  Y  Q  H

301 ATACTTTTGAAAAGGCGACTCCTGATAAAATGTACGGTTACAATAAGGAAAACGCCATCA  360
      T  F  E  K  A  T  P  D  K  M  Y  G  Y  N  K  E  N  A  I  T

361 CATATCAAACAGAGGATGGGCAAGTTCTCACAGACGTCCTTGCATTCTCTGACGACAATT  420
      Y  Q  T  E  D  G  Q  V  L  T  D  V  L  A  F  S  D  D  N  C

421 GCTATGTCATCTACGCTCTTGGCCCAGATGGAAGTGGAGCAGGTTACGAACTCTGGGCTA  480
      Y  V  I  Y  A  L  G  P  D  G  S  G  A  G  Y  E  L  W  A  T

                                T3b→  ←T7d
481 CCGATTACACGGATGTTCCAGCCAGTTGTCTAGAGAAGTTCAATGAGTATGCTGCAGGTC  540
      D  Y  T  D  V  P  A  S  C  L  E  K  F  N  E  Y  A  A  G  L

541 TGCCGGTACGGGACGTATACACAAGTGATTGCCTCCCAGAATAACTTGGGCATATCGTAA  600
      P  V  R  D  V  Y  T  S  D  C  L  P  E  *

601 TTTCAACTTCAAAGTGTGTTATTGTCAGCATATGTCTCGAGTGTTTGATGTAGTGCGTTC  660

661 GATGATGCCATTCATCTAGGTTTCGGGTGTTCGGTACTTTATGGTCACTGCCGACGGCCA  720
                                                        ←T7

721 GCACGAGTACTCGAAAATAAAGTATTCTGAAATCGGAAAAAAAAAAAAAAA          770
```

FIG. 2

FS-HBP2

```
T3→
   1  GCCGCGACGGAACTTCGAAGGAAGTCAGCATGAAGCTTCTCATACTCTCTCTTGCCCTCG   60
                                  M  K  L  L  I  L  S  L  A  L  V

  61  TCCTCGCCCTCAGCCAGGTTAAGGGAAATCAGCCAGATTGGGCCGATGAAGCGGCAAATG  120
      L  A  L  S  Q  V  K  G  N  Q  P  D  W  A  D  E  A  A  N  G
                                ↑

 121  GTGCACACCAAGACGCCTGGAAGAGTCTGAAAGCGGACGTTGAAAACGTTTACTACATGG  180
      A  H  Q  D  A  W  K  S  L  K  A  D  V  E  N  V  Y  Y  M  V

 181  TGAAGGCCACCTATAAGAATGACCCAGTGTGGGGCAATGACTTCACTTGCGTGGGTGTTA  240
      K  A  T  Y  K  N  D  P  V  W  G  N  D  F  T  C  V  G  V  M

                T3b→  ←T7a
 241  TGGCAAATGATGTCAACGAGGATGAGAAGAGCATTCAAGCAGAGTTTTTGTTTATGAATA  300
      A  N  D  V  N  E  D  E  K  S  I  Q  A  E  F  L  F  M  N  N

 301  ATGCTGACACAAACATGCAATTCGCCACTGAAAAGGTGACTGCTGTTAAAATGTATGGTT  360
      A  D  T  N  M  Q  F  A  T  E  K  V  T  A  V  K  M  Y  G  Y

 361  ACAATAGGGAAAACGCCTTCAGATACGAGACGGAGGATGGCCAAGTTTTCACAGACGTCA  420
      N  R  E  N  A  F  R  Y  E  T  E  D  G  Q  V  F  T  D  V  I

                                                  →
 421  TTGCATACTCTGATGACAACTGCGATGTCATCTACGTTCCTGGCACAGACGGAAATGAGG  480
      A  Y  S  D  D  N  C  D  V  I  Y  V  P  G  T  D  G  N  E  E

                ←
 481  AAGGTTACGAACTATGGACTACGGATTACGACAACATTCCAGCCAATTGTTTAAATAAGT  540
      G  Y  E  L  W  T  T  D  Y  D  N  I  P  A  N  C  L  N  K  F

 541  TTAATGAGTACGCTGTAGGTAGGGAGACAAGGGATGTATTCACAAGTGCTTGCCTAGAGT  600
      N  E  Y  A  V  G  R  E  T  R  D  V  F  T  S  A  C  L  E  *

            →                                     ←
 601  AATAACTTCAGAATGTCGTTCTTTCAAAGCGAAAAACCAACAATGTGAACATCGGCTTGC  660

 661  TGTGCTCGACGTAGCCAGCGATAATGTTGTTTTCCTGGGTTTCTGGGTTTGGATACTTTT  720

 721  AGCCACTGCCGAAGAGCTGTAAAGGTAATGAAAAATAAAATGTTCAAGAGTGTGAAAAAA  780

                ←T7
 781  AAAAAAAAAAAAA  793
```

FIG. 3

MS-HBP1

```
      T3→
1     AAAGCACTCAACATGAAGGTTCTTTTGTTGGTTCTTGGAGCTGCTCTTTGCCAGAATGCA   60
                M  K  V  L  L  L  V  L  G  A  A  L  C  Q  N  A

61    GATGCAAACCCAACATGGGCGAACGAAGCTAAATTGGGATCCTACCAAGACGCCTGGAAG  120
      D  A  N  P  T  W  A  N  E  A  K  L  G  S  Y  Q  D  A  W  K
            ↑

121   AGCCTTCAGCAAGACCAAAACAAGAGATACTATTTGGCACAAGCGACACAAACGACTGAC  180
      S  L  Q  Q  D  Q  N  K  R  Y  Y  L  A  Q  A  T  Q  T  T  D

                                  →
181   GGCGTATGGGGTGAAGAGTTTACTTGTGTGAGTGTTACGGCTGAGAAGATTGGAAAGAAA  240
      G  V  W  G  E  E  F  T  C  V  S  V  T  A  E  K  I  G  K  K

      ←
241   AAACTTAACGCTACGATCCTCTATAAAAATAAGCACCTTACTGACCTGAAAGAGAGTCAT  300
      K  L  N  A  T  I  L  Y  K  N  K  H  L  T  D  L  K  E  S  H

301   GAAACAATCACTGTCTGGAAAGCATACGACTACACAACGGAGAATGGCATCAAGTACGAG  360
      E  T  I  T  V  W  K  A  Y  D  Y  T  T  E  N  G  I  K  Y  E

361   ACGCAAGGGACAAGGACGCAGACTTTCGAAGATGTCTTTGTATTCTCTGATTACAAGAAC  420
      T  Q  G  T  R  T  Q  T  F  E  D  V  F  V  F  S  D  Y  K  N

            →                                           ←
421   TGCGATGTAATTTTCGTTCCCAAAGAGAGAGGAAGCGACGAGGGCGACTATGAATTGTGG  480
      C  D  V  I  F  V  P  K  E  R  G  S  D  E  G  D  Y  E  L  W

481   GTTAGTGAAGACAAGATTGACAAGATTCCCGATTGCTGCAAGTTTACGATGGCGTACTTT  540
      V  S  E  D  K  I  D  K  I  P  D  C  C  K  F  T  M  A  Y  F

                  →
541   GCCCAACAGCAGGAGAAGACGGTTCGTAATGTATACACTGACTCATCATGCAAACCAGCA  600
      A  Q  Q  Q  E  K  T  V  R  N  V  Y  T  D  S  S  C  K  P  A

601   CCAGCTCAGAACTGATATTCTGGTAATGCTTGAACCGTAATGGTTCGACCTGCAGTCTAG  660
      P  A  Q  N  *

661   AAACATTTACCACCATCACGGTGATTATCTTACCGTAGTTTCTTAGGTCTTTGTTCTTTGA  720

                                                  ←T7
721   ATAAAATAGTTCCCTGCATTGACAAAAAAAAAA  753
```

FIG. 4

```
T3→
   1  ATGAAGATGCAGGTAGTGCTCTTACTTACCTTTGTTAGCGCCGCCCTCGCCACTCAAGCG   60
   1  M  K  M  Q  V  V  L  L  L  T  F  V  S  A  A  L  A  T  Q  A    20

  61  GAGACTACATCTGCGAAAGCAGGAGAAAACCCGCTCTGGGCGCATGAGGAACTACTTGGA  120
  21  E  T  T  S  A  K  A  G  E  N  P  L  W  A  H  E  E  L  L  G    40
                              ↑

 121  AAATATCAAGATGCCTGGAAAAGCATCGATCAGGGCGTGTCGGTGACTTATGTCCTTGCA  180
  41  K  Y  Q  D  A  W  K  S  I  D  Q  G  V  S  V  T  Y  V  L  A    60

                        →                       ←
 181  AAGACAACATATGAGAATGACACAGGATCATGGGGATCCCAGTTTAAGTGCCTCCAGGTA  240
  61  K  T  T  Y  E  N  D  T  G  S  W  G  S  Q  F  K  C  L  Q  V    80

 241  CAAGAAATAGAAAGAAAGGAAGAAGACTATACAGTTACATCTGTTTTCACCTTTAGAAAT  300
  81  Q  E  I  E  R  K  E  E  D  Y  T  V  T  S  V  F  T  F  R  N   100

 301  GCGTCTTCTCCAATCAAGTATTACAACGTGACAGAAACAGTGAAGGCCGTTTTTCAATAT  360
 101  A  S  S  P  I  K  Y  Y  N  V  T  E  T  V  K  A  V  F  Q  Y   120

 361  GGATACAAAAACATAAGGAATGCAATTGAATACCAAGTGGGCGGTGGACTTAACATAACC  420
 121  G  Y  K  N  I  R  N  A  I  E  Y  Q  V  G  G  G  L  N  I  T   140

                        →       ←
 421  GACACGCTCATTTTCACTGATGGAGAATTATGCGATGTTTTCTATGTTCCCAATGCAGAT  480
 141  D  T  L  I  F  T  D  G  E  L  C  D  V  F  Y  V  P  N  A  D   160

 481  CAAGGTTGTGAGCTCTGGGTCAAAAAGAGTCACTACAAACACGTACCAGACTACTGCACG  540
 161  Q  G  C  E  L  W  V  K  K  S  H  Y  K  H  V  P  D  Y  C  T   180

 541  TTCGTGTTCAATGTTTTCTGTGCGAAAGACAGGAAAACCTACGATATATTTAATGAAGAA  600
 181  F  V  F  N  V  F  C  A  K  D  R  K  T  Y  D  I  F  N  E  E   200

 601  TGTGTTTATAACGGCGAACCCTGGCTTTAAAGGCAAAAAATCTATAAAATACGGTTTCTG  660
 201  C  V  Y  N  G  E  P  W  L  *                                  220

                                                                  ←T7
 661  TAGTAAGTACTAATAGCAAGTAGTTGAATAATAAAAAGATTGTAAGTGCAAAAAAAAAA  719
```

FIG. 5

Ra-Res

```
1    CAACTGATCACTAAAATGTTCCTTGCGGGTTTCTTCATTTTCGGCGCTGCCGTCCTCTCA   60
                  M  F  L  A  G  F  F  I  F  G  A  A  V  L  S

61   GTTTTGGCTGAGGAGACACCTAATGATAGATGTACTACACACACTCCTAATGGATGGCAG   120
     V  L  A  E  E  T  P  N  D  R  C  T  T  H  T  P  N  G  W  Q

121  TTTCTCAAGAAAGGCAAGAGATACGATATGAAACAGAGAACCTTCCAAACACCTAACTCA   180
     F  L  K  K  G  K  R  Y  D  M  K  Q  R  T  F  Q  T  P  N  S

181  GACGACACTAAATGCCTGTCCAGTACTATCGACGGAAAGAATGAAAATAACCATACAGTA   240
     D  D  T  K  C  L  S  S  T  I  D  G  K  N  E  N  N  H  T  V

241  CAAGCAACGATAAGATATCGAAATGGTTATGAAGGAAAATGGGACACCATCCGCCAGGAG   300
     Q  A  T  I  R  Y  R  N  G  Y  E  G  K  W  D  T  I  R  Q  E

301  TACGAGTTCCCCAACTACACTGCAGGAGACTACAACTCCATGAAGACAACAGACAAATCC   360
     Y  E  F  P  N  Y  T  A  G  D  Y  N  S  M  K  T  T  D  K  S

361  CCGCCTCCGCCGGCATCATACCTGTTTGGATATACTGGAAGCTCTTGTGCCGTGGTGTAC   420
     P  P  P  P  A  S  Y  L  F  G  Y  T  G  S  S  C  A  V  V  Y

421  GTGAATTCCATTGGACCTGTTCGTAGCAATTCTGAAAACCCACCAGAAAGACTCACAGCA   480
     V  N  S  I  G  P  V  R  S  N  S  E  N  P  P  E  R  L  T  A

481  AGTCAGGAAAGTGCACAACGCGATTGCGTCCTTTGGGTCGATCACGATGAAAAAGCTACC   540
     S  Q  E  S  A  Q  R  D  C  V  L  W  V  D  H  D  E  K  A  T

541  CAAGAACAATGCTGTGAAGATTTCTTCAAGACCCACTGCAAAGAGACTGTCCATGTCATA   600
     Q  E  Q  C  C  E  D  F  F  K  T  H  C  K  E  T  V  H  V  I

601  TACGACGTGAATAGATGCAAGGAGAATGGCAGTGAATAACACGATGCCGGGAATGGCATG   660
     Y  D  V  N  R  C  K  E  N  G  S  E  *

661  GCGACTTCATTTATGAAGGAAGACTTCCACAGATGTGAAACTTGCCTTCATTTTGCTTGT   720

721  TACTTTAGACCAACATATTCTTCCTTTTCCGACTTCAATGATATGATCTAGGTTGTAAAA   780

781  AGAGCGTTTTAATAAAGAAAGTATTAGCATCGATGATGGAAATATAAAAAAA   832
```

Av-HBP

FIG. 6

```
1   GCGACCGCGCCCAGCCGTACAGAACAAATAGCCTTCGTTGCAAACGTGCAGCGTAGTCGG   60

61  ATGCCTAGTTAAACACCACACACACGTAAAAAGTAGACGAAACTGGCTTCGCTTCCAGCA   120

121 CCAAGCAGGTCATCGTCTGGTCCACTGACGATGAACTCTGCCTTGTGGGTTTTACTAGGA   180
                                  M  N  S  A  L  W  V  L  L  G

181 TCATCCTTATGGCTGCATACGGTAGCGTTCATGATTCCCACATGGGCAGATGAAGGCAGG   240
    S  S  L  W  L  H  T  V  A  F  M  I  P  T  W  A  D  E  G  R

241 TTTGGCAAGTACCAGAACGCCTGGAAGGCCCTGAATCAGCGGATTAACACAACACATGTC   300
    F  G  K  Y  Q  N  A  W  K  A  L  N  Q  R  I  N  T  T  H  V

301 CTTGTGAGGTCAACGTATATCGACAATCCATATTTATGGGGCAAGAACTTCTCATGCGTA   360
    L  V  R  S  T  Y  I  D  N  P  Y  L  W  G  K  N  F  S  C  V

361 CGCGCTCGAACTGTCGAAGTCTTTCCCAGCAGCAAGACTGTGGAACTGGAGTTTAGTTTC   420
    R  A  R  T  V  E  V  F  P  S  S  K  T  V  E  L  E  F  S  F

421 AGAAACAGGACTGGTATATTGTGCATGAGAAATCAAACGGTTCGAGCTGGAAAGGATTAC   480
    R  N  R  T  G  I  L  C  M  R  N  Q  T  V  R  A  G  K  D  Y

481 TTTTATCATCAGCCTAACGCCTTCGAATTCATGCTGAGAGGTAACAGGTCGTTTTCTAAC   540
    F  Y  H  Q  P  N  A  F  E  F  M  L  R  G  N  R  S  F  S  N

541 GCTGTCATGTTTACCGACGGAATGACATGTAATCTGCTCAGCTTTCCATACCAGCGCAAC   600
    A  V  M  F  T  D  G  M  T  C  N  L  L  S  F  P  Y  Q  R  N

601 AAACCACAATGCGAACTATGGGTGAAGGACACGCGCGTCGACAACATTCCCCCTTGTTGC   660
    K  P  Q  C  E  L  W  V  K  D  T  R  V  D  N  I  P  P  C  C

661 TCGTTCATGTTCGACTATTTGTGCCCACAGCCTCGTCCATTCATCATTTACGACAAAGCA   720
    S  F  M  F  D  Y  L  C  P  Q  P  R  P  F  I  I  Y  D  K  A
```

```
721  ATGTGCACGGTGAGGCCACCCCGCTAGAAAGAAAAGGGATGAAAAGGCTACTCGAAGAAG   780
     M  C  T  V  R  P  P  R  *

781  CAACAACCAATCAGTGCCCACAAGAGAACCGTTCCAGTCCTGCGAAAGTTGCGCCTCCCA   840

841  AAACACATACATTTCACTGCAAAGATGACCGATGCAGTCGCAAATTCGTGTCCTAGAACT   900

901  CAAGTGCTGTTTTGGAAACTCGGAAAGGAGACAGTAGAAGCTAACTGCTGTGATACCTAG   960

961  GCCAGGCATTTCCGTCGGGCACTGTTTTTTATGAATAGGGTAGGGTGAAAGTATTTTGGC  1020

1021 TTTGCTGTGGCCCAATAAATAGCGTATATTAGCGGACTAGCATCGAAGTTCCAGATGCTA  1080

1081 TAAAGCAGCTAAAACTCACTTCTGCCTGGAACTTCGATAGGTATTGAATAGATCATGCGC  1140

1141 GCACAGAAAAGAAAAGTATCAATCAAAACATAAAAAGCATTCTTCGCATGTGCGCAAAGC  1200

1201 ATTCCCTAAGTCCACGCTAAAAATAGGTGTCATTTCATATAGCATCGAGTTCTATACGTT  1260

1261 CTTAAGATGCTACCGGTCATTCATTCCTTTCTCGTCTATGCCTCATGGATCTGAACCAAG  1320

1321 TTCTTCTATTGCCTCCTTGTTTTCCGGTAGCTACAGAGTTCAGCAGCACCATTGCTAGTG  1380

1381 CATATTTTATCTTCGTGCTGTGTTTGTCGCAGTATATTTTTCTGCCTATTCACGATATTT  1440

1441 GCACAATGTAATAAAACATTTGCCTGCCTAAAAAAAAAAAAAAAAAAA              1488
```

FIG. 6(contd.)

FIG. 7

Ih/Bm-HBP1

```
1   CTCCAGCTCTGCTTCGACGATGAAGGCTCTCCTGATCGCTGTCGGCTACCTGGCTGCCGT   60
                M  K  A  L  L  I  A  V  G  Y  L  A  A  V

61  CACAGCGGCACCCCAAGCTTCGCCTTCCTCTCCGAGGAACGAACCACTCAAGAATACTAC  120
     T  A  A  P  Q  A  S  P  S  S  P  R  N  E  P  L  K  N  T  T

121 GTGGCACAGCAAGGAACTGAAAAATTATCAAGATGCGTGGAAGTCCATCAATCAAAACGT  180
     W  H  S  K  E  L  K  N  Y  Q  D  A  W  K  S  I  N  Q  N  V

181 CAGCACTACCTACTACTTCCTCAGATCAACCTACAACAACGACAGTGTCTGGGGTAAAAA  240
     S  T  T  Y  Y  F  L  R  S  T  Y  N  N  D  S  V  W  G  K  N

241 TTTCACCTGTCTTAGCGTCACGGTGACATCGAAACATGAATCAACGTTCACCGTCGAATA  300
     F  T  C  L  S  V  T  V  T  S  K  H  E  S  T  F  T  V  E  Y

301 TAACACCACGTACAAAAATCAGAGCCAACAATGGGTCAGCATGACGGAAAACGTCACGGC  360
     N  T  T  Y  K  N  Q  S  Q  Q  W  V  S  M  T  E  N  V  T  A

361 CGTGCAGGAGGAGGGCTACGACGTTAAAAATATCATTCAGTGGACAACAGAGAATAACAC  420
     V  Q  E  E  G  Y  D  V  K  N  I  I  Q  W  T  T  E  N  N  T

421 AAAGTTCAATGATACTGTTGTTTTTACGGACGGCCAGACTTGTGATCTGTTGTACATCCC  480
     K  F  N  D  T  V  V  F  T  D  G  Q  T  C  D  L  L  Y  I  P

481 GTACAAAGAAAACGGTTACGAGCTGTGGGTGCGTTCGGATTACCTGCAGAACACTCCAAC  540
     Y  K  E  N  G  Y  E  L  W  V  R  S  D  Y  L  Q  N  T  P  T

541 GTGCTGCCAGTTCATCTTTGACCTCGTCGCATTGGGACGTACCACGTACAATATCTCCAC  600
     C  C  Q  F  I  F  D  L  V  A  L  G  R  T  T  Y  N  I  S  T

601 TCCTGACTGCGTGACCAAAACCTCTCGTTAGACCGTGAAAGCCGCGGCTTATGCTACTCG  660
     P  D  C  V  T  K  T  S  R  *

661 ACTGCTCAGGTTGGAAGAGTAGGGAGCCCCGACGCGCACTACTACTAAAAATGATTCCAA  720

721 ATAAAGTATTCAAACATTTCAAAAAAAAAAAAAAAAAAAA                      760
```

Ih/Bm-HBP2

FIG. 8

```
   1  AGTGACTCCTGCTCTGCTTCGACGATGAAGGCTCTCCTGATCGCTGTCGTCTACCTGACT   60
                              M  K  A  L  L  I  A  V  V  Y  L  T

  61  GCCGTCACAGCGGCAGACCAAGCTCCGCCTTCCTCTACGAGGAATGAACCACTCGAGAAA  120
      A  V  T  A  A  D  Q  A  P  P  S  S  T  R  N  E  P  L  E  K

 121  ACTACCTGGCACAACCAGACACTGGGACGTTATCAAGATGCGTGGAAGTCCATCAATCAA  180
      T  T  W  H  N  Q  T  L  G  R  Y  Q  D  A  W  K  S  I  N  Q

 181  AGCGTCGGCACTACCTACTACTTCCTCAGATCAACCTACAACAACGACAGCGTGTGGGGT  240
      S  V  G  T  T  Y  Y  F  L  R  S  T  Y  N  N  D  S  V  W  G

 241  AAAAATTTCACCTGTCTTAGCGTCACGGTGACATCGAAATATGAATCAACGTTCACCGTC  300
      K  N  F  T  C  L  S  V  T  V  T  S  K  Y  E  S  T  F  T  V

 301  GAATATAACACCACGTACAAAAATCAGAGCCAACAATGGGTCAGCATGTCGGAAAACGTC  360
      E  Y  N  T  T  Y  K  N  Q  S  Q  Q  W  V  S  M  S  E  N  V

 361  ACGGCCGTGCAGGAGGGCGGCTACAGTGTTAAAAACATCATTCAGTGGACAACGGAGAAT  420
      T  A  V  Q  E  G  G  Y  S  V  K  N  I  I  Q  W  T  T  E  N

 421  AACACAAAGTTCAATGATACTGTTGTTTTTACGGACGGCCAGACTTGTGATGTGTTATAC  480
      N  T  K  F  N  D  T  V  V  F  T  D  G  Q  T  C  D  V  L  Y

 481  ATCCCGTACAAAGAAGACGGTTACGAGCTGTGGGTGCGTTCGGAATACCTGCAGAACACT  540
      I  P  Y  K  E  D  G  Y  E  L  W  V  R  S  E  Y  L  Q  N  T

 541  CCAACGTGCTGCCAGTTCATCTTTGACCTCGTCGCATTGGGACGTACCACGTACAATATC  600
      P  T  C  C  Q  F  I  F  D  L  V  A  L  G  R  T  T  Y  N  I

 601  TCCACTCCTAACTGCGTGGCCACCACCGCTGGTTAGACAATGCAAGCCGCGGCTTAATTT  660
      S  T  P  N  C  V  A  T  T  A  G  *

 661  ACTCGACCGCTCAGGTTGGAAGTGCCGGGAGCCTCGACGGGCACTACTACTTAAAATGAT  720

 721  TTCGAATAAAGTATTCAAGCATTTCTGGAAAAAAAAAAAAAAAAA  765
```

Ih/Bm-HBP-3

```
1   GATGGCGCTCAGATTTGCACTTCTGCTGGCGTGCATCGTCACGGCATGTGGCTGGAGAAC   60
      M  A  L  R  F  A  L  L  L  A  C  I  V  T  A  C  G  W  R  T

61  ACGGATTCAAGAGAAAGGTCCCGAGAACAACCCTCTCATGAACACCCAACGTTTGGGAAA  120
      R  I  Q  E  K  G  P  E  N  N  P  L  M  N  T  Q  R  L  G  K

121 AATGCAAGACGCATGGAAGAGTCTGGAAAAGGCAACAAATCAGTCGTATGTCTTGGTGTT  180
      M  Q  D  A  W  K  S  L  E  K  A  T  N  Q  S  Y  V  L  V  F

181 CCGCTCAAGAAATCACGAACCAGAGATATCCTGCGTGTACGTGAGGGCTAGTAATATAAA  240
      R  S  R  N  H  E  P  E  I  S  C  V  Y  V  R  A  S  N  I  N

241 TAATGACACTAAAACTGCAACTTATACCAGAACATATTACAATATGACGGCAAACGCAAC  300
      N  D  T  K  T  A  T  Y  T  R  T  Y  Y  N  M  T  A  N  A  T

301 CATGACGGTGAATTATACTGCAAGAGCTCTGAAGCAAGTGGACTATGAGTCGGAAAATGT  360
      M  T  V  N  Y  T  A  R  A  L  K  Q  V  D  Y  E  S  E  N  V

361 CGTACGAGTAAACCTGACAGGTGGGGTCCCCAGCAACGATACAGTTCCTCTTGGAAGCTA  420
      V  R  V  N  L  T  G  G  V  P  S  N  D  T  V  P  L  G  S  Y

421 CGAATACGTCGAGTACGGTAATTACTCCTGCAATAGCTCATCGACACCCTTTTTGGATGC  480
      E  Y  V  E  Y  G  N  Y  S  C  N  S  S  S  T  P  F  L  D  A

481 TGTGCAAATGGCATCGCAAGGGCAATCCAGAGGGCCGGATATCGAAGGGCGCACATATCT  540
      V  Q  M  A  S  Q  G  Q  S  R  G  P  D  I  E  G  R  T  Y  L
```

FIG. 9

FIG. 9 (CONTD.)

```
541  AGACTTCTACGTCGTCTACAATCAACCATCGTGCAATGTCCTGAAGTCCCCGCTCCTGGG   600
       D  F  Y  V  V  Y  N  Q  P  S  C  N  V  L  K  S  P  L  L  G

601  AGGTGCTTGTGACTTTTGGGTGACAGAATCCGAGTTGCAAAAAGCACTAAATAAGACATC   660
       G  A  C  D  F  W  V  T  E  S  E  L  Q  K  A  L  N  K  T  S

661  AGAGAAGAAAAAAACAAAGCTAGAAGCGAGAGCAAGGAAAGCTGGAGGAGATTCCGATGA   720
       E  K  K  K  T  K  L  E  A  R  A  R  K  A  G  G  D  S  D  D

721  CCAGGGACCTGAACTGGAGGTCGTCTTCAAAAATCTGCCCCCTCCCTGCCGCGCAGCGTT   780
       Q  G  P  E  L  E  V  V  F  K  N  L  P  P  P  C  R  A  A  F

781  CATAACTTCCTGCGGCTATCCAACTTTTCTTATGTACAACAAGACCATCTGTAATCGAAC   840

       I  T  S  C  G  Y  P  T  F  L  M  Y  N  K  T  I  C  N  R  T

841  GGATTCTGCTGCGGTGTGAACGTCCCCTGCGAGCAAGTAGAACGTCCGTGAAGACAGCAG   900
       D  S  A  A  V  *

901  GAAGATAGTTGACTGTTTTGTTGGCGGAATGTGACTACTAGTCTGAATCATTAAAAAGAT   960

961  TCNGCTGACGGGTGTGGCGGGAACTTTTTTAAATGAAATTGGTCATACTTGTTGAAAGAC   1020

1021 AAAAATAAAACAATATGTTACTCCTC  1046
```

Ih/Bm-HBP4

FIG. 10

```
1   GGAAACCAGGATGGCGCTCAGATTTGCACTTCTGCTGGCGTGCATCGTCACGGCATGTGG   60
              M  A  L  R  F  A  L  L  L  A  C  I  V  T  A  C  G

61  CTGGAGAACACGGATTCAAGAGAAAGGTCCCGAGAACAACCCTCTCATGAACACCCAACG  120
      W  R  T  R  I  Q  E  K  G  P  E  N  N  P  L  M  N  T  Q  R

121 TTTGGGAAAAATGCAAGACGCATGGAAGAGTCTGGAAAAGGCAGCAAATCAGACGTATGT  180
      L  G  K  M  Q  D  A  W  K  S  L  E  K  A  A  N  Q  T  Y  V

181 CTTGGTGTTCCGCTCAAGAAATCACGAACCAGATATATCCTGCGTCTACGTGAGAGCTAG  240
      L  V  F  R  S  R  N  H  E  P  D  I  S  C  V  Y  V  R  A  S

241 TAATTTAGATAATGCAACTAAAACTGCAGATTATACCAGAACATATTACAATATGACGGC  300
      N  L  D  N  A  T  K  T  A  D  Y  T  R  T  Y  Y  N  M  T  A

301 AAAACAAAACGTGTCGGTAAATTATACTGCAAGAGCTCTGAAGCAAGTGGACTATGAGTC  360
      K  Q  N  V  S  V  N  Y  T  A  R  A  L  K  Q  V  D  Y  E  S

361 GGAAAATGTCGTACGAGTAAACCTGACAGGTGGGGTCCCCAGTAACGATACAGTTCCTCC  420
      E  N  V  V  R  V  N  L  T  G  G  V  P  S  N  D  T  V  P  P

421 TGGAAGCTTCGAATACGTCGAGTACGGTAATTACTCCTGCAATAGCTCATCGACACCCTT  480
      G  S  F  E  Y  V  E  Y  G  N  Y  S  C  N  S  S  S  T  P  F

481 TTTGGATGCTGTGCAAATGGCATCGCAAGGGCAATCCTGGGGGCCGGATGTCGAAGGGCG  540
      L  D  A  V  Q  M  A  S  Q  G  Q  S  W  G  P  D  V  E  G  R
```

```
541  CACATATCTAGATTTCTACGTCGTCTACAATCAACCGTCGTGCAATGTCCTGAAGTCCCC  600
       T  Y  L  D  F  Y  V  V  Y  N  Q  P  S  C  N  V  L  K  S  P

601  GCTCCTGGGAGGTGCTTGTGACTTCTGGGTGCCACAATCAGAGTTGGACAAGGTACTAAA  660
       L  L  G  G  A  C  D  F  W  V  P  Q  S  E  L  D  K  V  L  N

661  CAAAAAAGGAGATAAGAAAAAGCCAGCTAAGTCAAGCAGTCAAAATGGAGACGAAGGTTC  720
       K  K  G  D  K  K  K  P  A  K  S  S  S  Q  N  G  D  E  G  S

721  TGATGCCGAGCAACCTGAACTGGAGGCCATCTTTAAACATCTACCCCCTCCCTGCCGCGC  780
       D  A  E  Q  P  E  L  E  A  I  F  K  H  L  P  P  P  C  R  A

781  AGCGTTCATAACTTCCTGCGGCTATCCAAATTTTCTCATGTACAACAAGACGATCTGTAA  840
       A  F  I  T  S  C  G  Y  P  N  F  L  M  Y  N  K  T  I  C  N

841  TGCAGCGGGTCATGCTGCGAACTGAACGTCCTCTGCGAACGAGTAGAGCGTGCGTAAAAA  900
       A  A  G  H  A  A  N  *

901  CAACTGGTCTGAATCTTTTAAGAAATTCGGCAAAGTGCGGGTGGCGCGAACTTTTATCAA  960

961  ACTGGTCATACATGTGAAAGAAAAAAATAAAACAAAATGTGCATAAAAAAAAAAAAAAAA  1020

1021 AAAAA  1025
```

FIG. 10(contd.)

FIG. 11

Ih/Bm-HBP-5

```
1   CGAAGAGCAGGTACGATTCGAATCTTTGCAATGGACATTCGCAGCGCTGTTTTGTTCGCG   60
                                M  D  I  R  S  A  V  L  F  A

61  TGCATCGTCTCGGCGTGTTGTGGCTTTTGGCGCTGGACAACACGGAGGGTAACTAAAAAG  120
    C  I  V  S  A  C  C  G  F  W  R  W  T  T  R  R  V  T  K  K

121 CCTGATAACAGCCCTCTGTTGAACAACCAACATCTTGGTCTTTTCCAGGACGCATGGAAG  180
    P  D  N  S  P  L  L  N  N  Q  H  L  G  L  F  Q  D  A  W  K

181 ACTATAGAAGAGACGTCCAATGATACGTATGTCCTGATGTTCCGCTCAAAACATTACGAC  240
    T  I  E  E  T  S  N  D  T  Y  V  L  M  F  R  S  K  H  Y  D

241 CACGAGAACAAGGCTAAATGTGTCTTCGTAACGGCAAATATTACTGACTCCCGGAACAAA  300
    H  E  N  K  A  K  C  V  F  V  T  A  N  I  T  D  S  R  N  K

301 ACTGCCAATTACACAATAACGTATTACGATACTACAACAAATACATCCAACAATTTTACA  360
    T  A  N  Y  T  I  T  Y  Y  D  T  T  T  N  T  S  N  N  F  T

361 ATCCCAGTGAGAGCTCTGAACCAAACTGACTACTCACTAGAAAATGTGATTCGAGCAAGC  420
    I  P  V  R  A  L  N  Q  T  D  Y  S  L  E  N  V  I  R  A  S

421 TTCAACGGCGACACTCCAAGCTCTACTCCAGCCCCTCCCGGAAGCAGCGTGTACATTCAG  480
    F  N  G  D  T  P  S  S  T  P  A  P  P  G  S  S  V  Y  I  Q

481 TATAATAATGTTACCTGCTACGCCCAATATCACCCATTTTCAAATAATGGAATCAGTGCA  540
    Y  N  N  V  T  C  Y  A  Q  Y  H  P  F  S  N  N  G  I  S  A
```

FIG. 11 (CONTD.)

```
541  AAATATGATGAAATGCCCCGGGATGGCCGAAATTACTTGTTCGACAATTTTATTGGTGCT  600
     K  Y  D  E  M  P  R  D  G  R  N  Y  L  F  D  N  F  I  G  A

601  TACTTGGACTTCTACGTGGTGTTCAGCCAGCCGACATGCAACGTTCTCAGAGTCCGAGAA  660
     Y  L  D  F  Y  V  V  F  S  Q  P  T  C  N  V  L  R  V  R  E

661  GGATGTGACTTCTGGCTAAGGAAAACTGAGTTGCCAAGCCTACTGAAAGCAGCAGAAAAT  720
     G  C  D  F  W  L  R  K  T  E  L  P  S  L  L  K  A  A  E  N

721  GATGACAACGATAACACGGAATCGCTGAAGAACTATTGGGAAAGAAGAATAAATAATACT  780
     D  D  N  D  N  T  E  S  L  K  N  Y  W  E  R  R  I  N  N  T

781  AAAACAAGATTTCGACATAATACTAAGAAATGTAAGATGTACGTACAACGTTATTCAATT  840
     K  T  R  F  R  H  N  T  K  K  C  K  M  Y  V  Q  R  Y  S  I

841  GAGAAGGCTGAAGATGTCTTTAAAAACACTGCTTTTAAACACCTCCCCTCCGACTGCCGC  900
     E  K  A  E  D  V  F  K  N  T  A  F  K  H  L  P  S  D  C  R

901  TTTGCCTTCCTGGCCGCTTGTGGAAATCCAGCATTCACAATATACGACCCAGAAACATGT  960
     F  A  F  L  A  A  C  G  N  P  A  F  T  I  Y  D  P  E  T  C

961  AATAGCTCCCTGCCAGCTAATATGGCAGAAAGTTAAATGAGCTATTTCACTTCATGTTCG  1020
     N  S  S  L  P  A  N  M  A  E  S  *

1021 ACCGTATGCCTGGTATGCAAGAAGGTGAGGTTGGACAGGATACTTCCGAATTATTTTTTC  1080

1081 AGTCTGCCTTGTACGCACGAAATAACAAAATATCTGTTGAAGCCNNCAACNNNNNNAANA  1140

1141 ANAAAAAANAAAAAAA  1156
```

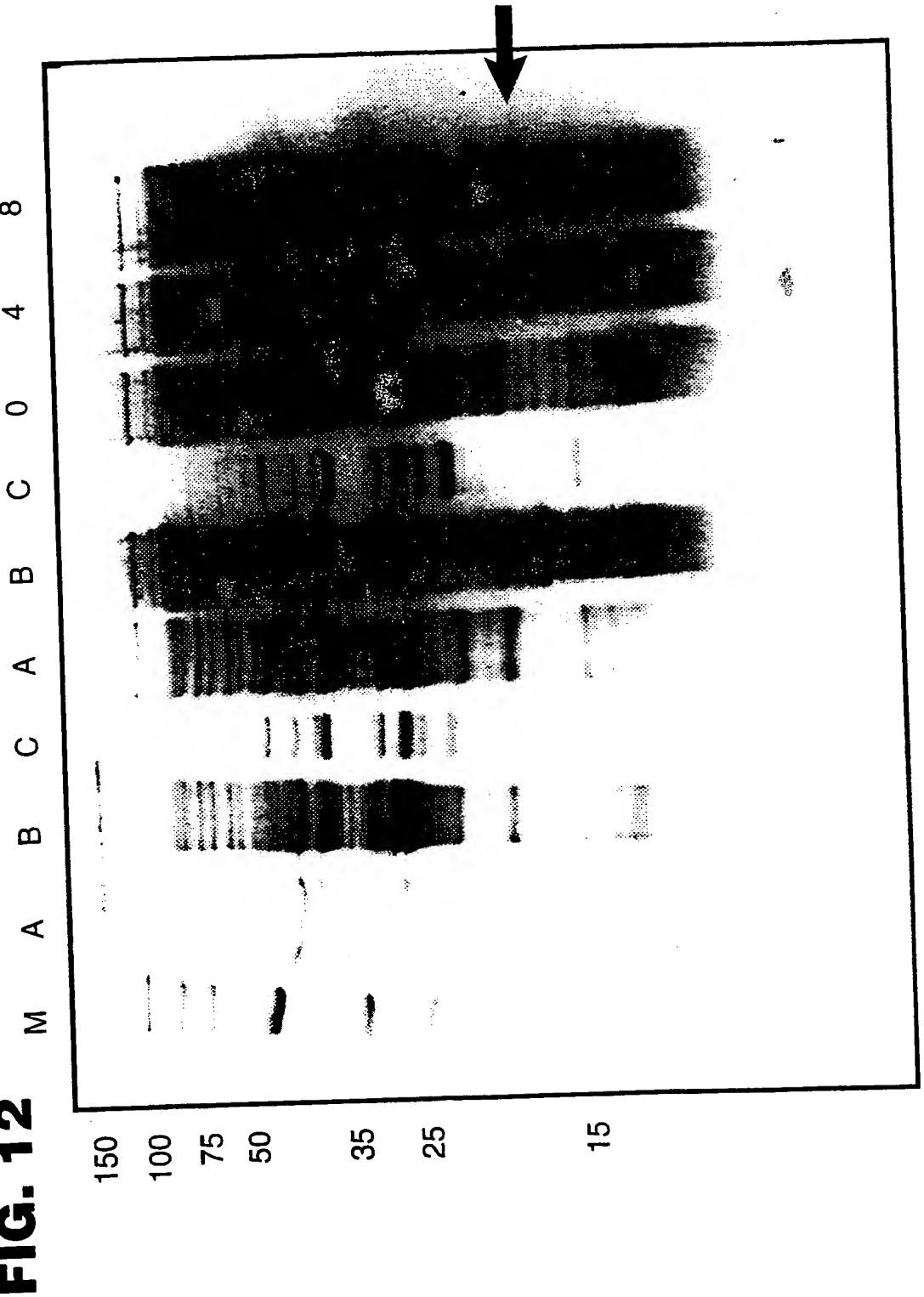

M
PRE-IPTG INDUCTION
A
B
C
POST-IPTG INDUCTION
A
B
C
TIME COURSE OF EXPRESION (HOUR)
0
4
8
150
100
75
50
35
25
15

FIG. 12

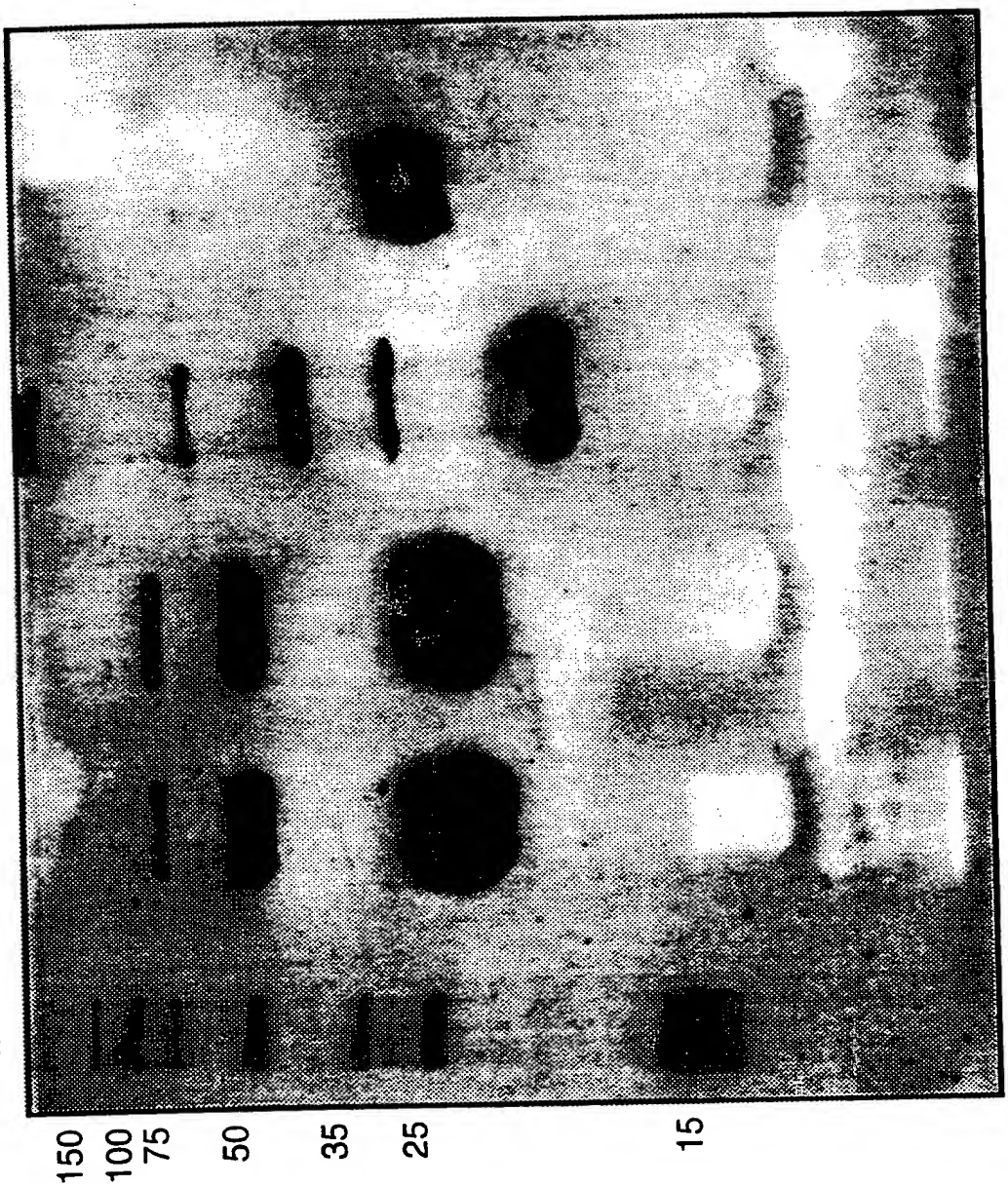


FIG. 13

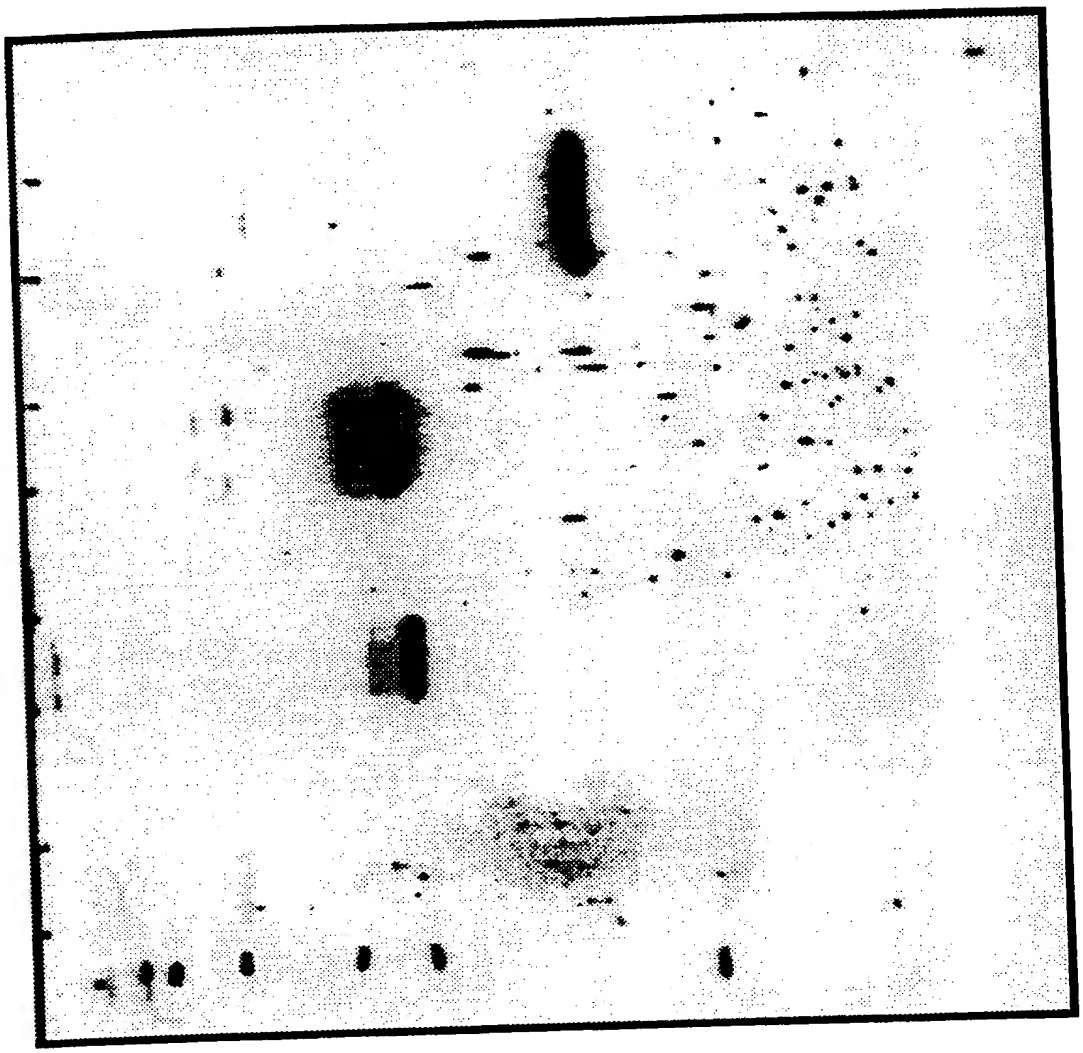


FIG. 14

FIG. 15

Binding Activity of derretine to histamine and its methylsubstitutions

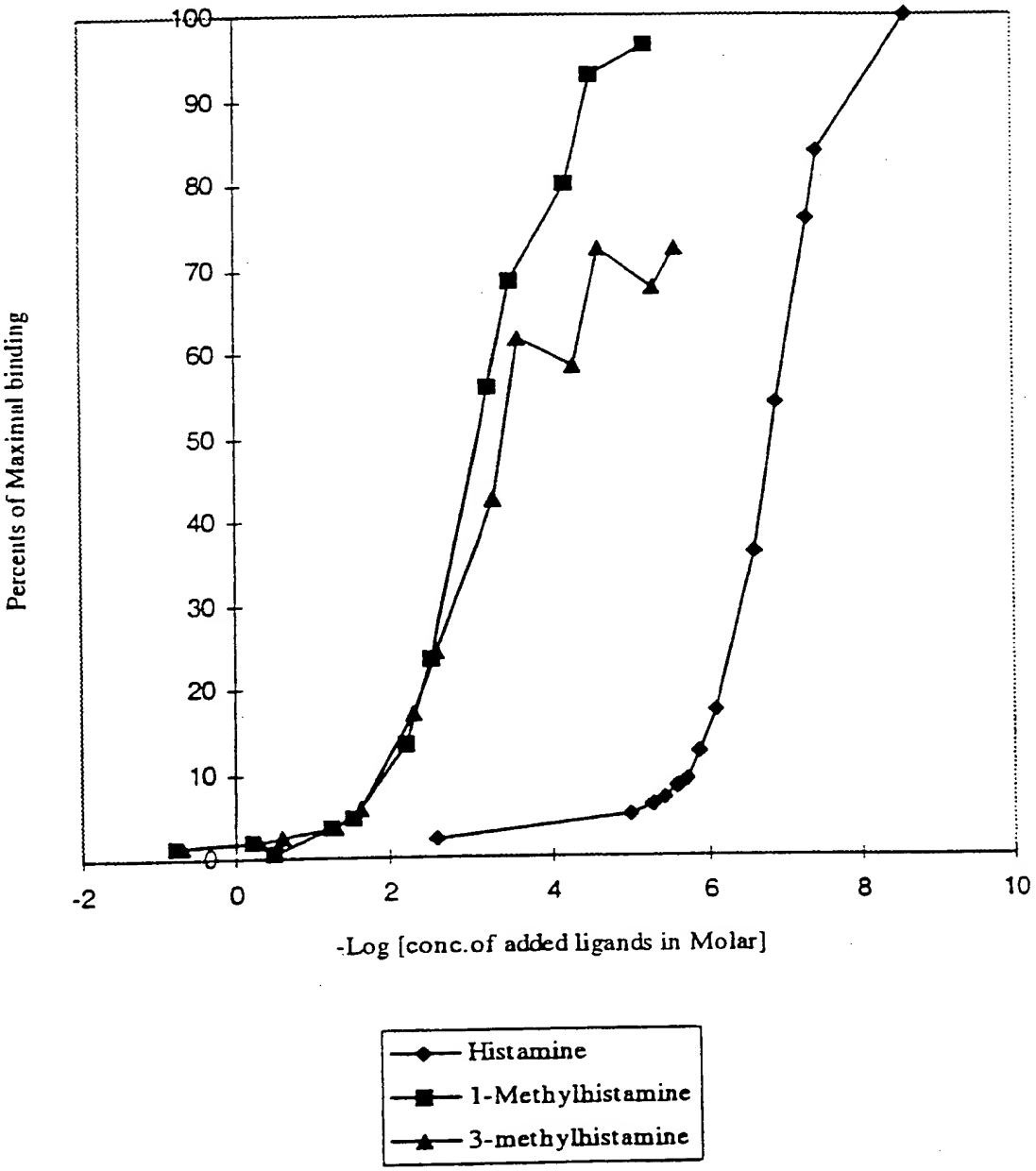
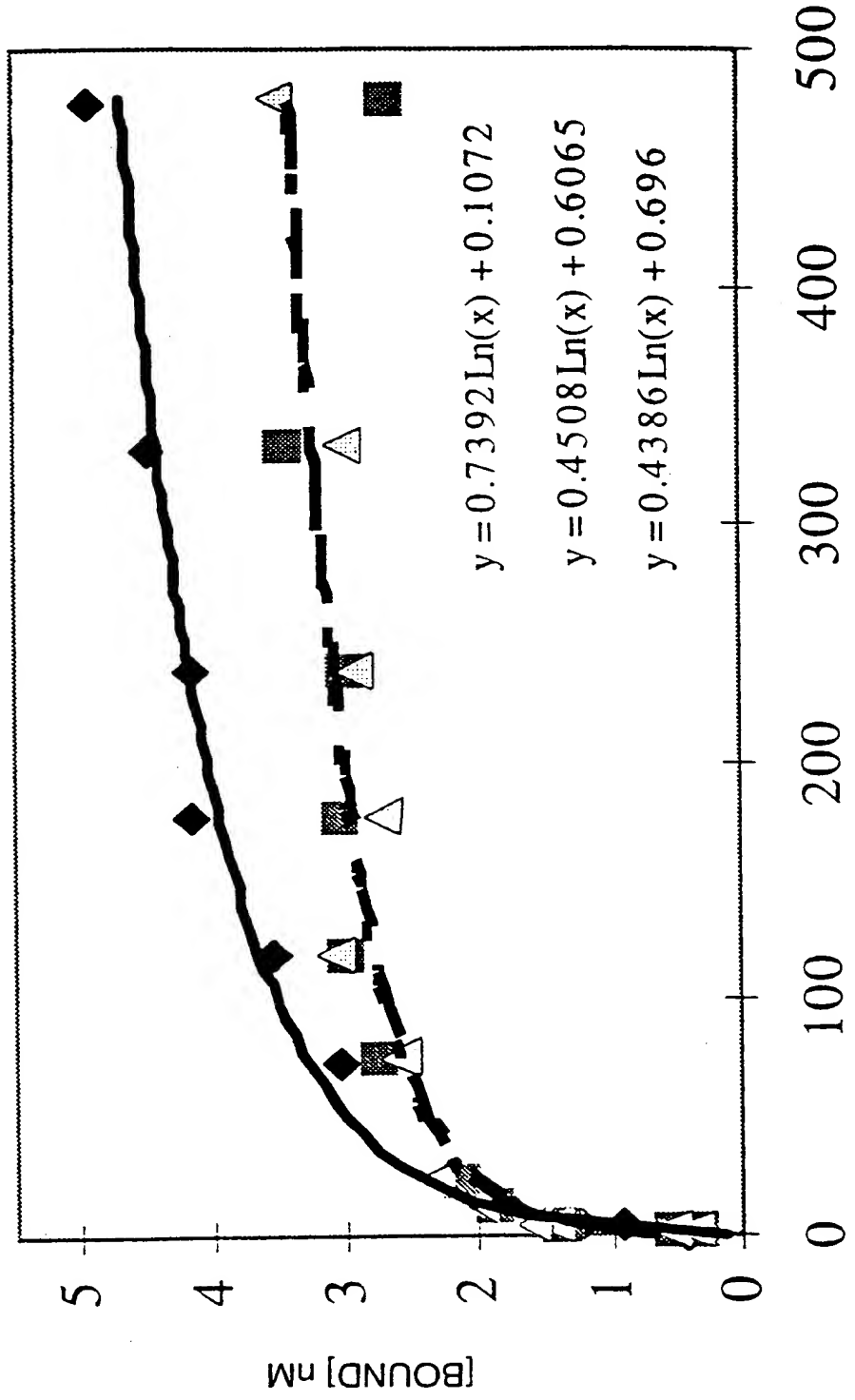


FIG. 16


Histamine-binding saturation curve
[BOUND] nM
[Free histamine] nM
y = 0.7392Ln(x) + 0.1072
y = 0.4508Ln(x) + 0.6065
y = 0.4386Ln(x) + 0.696
0
1
2
3
4
5
0
100
200
300
400
500

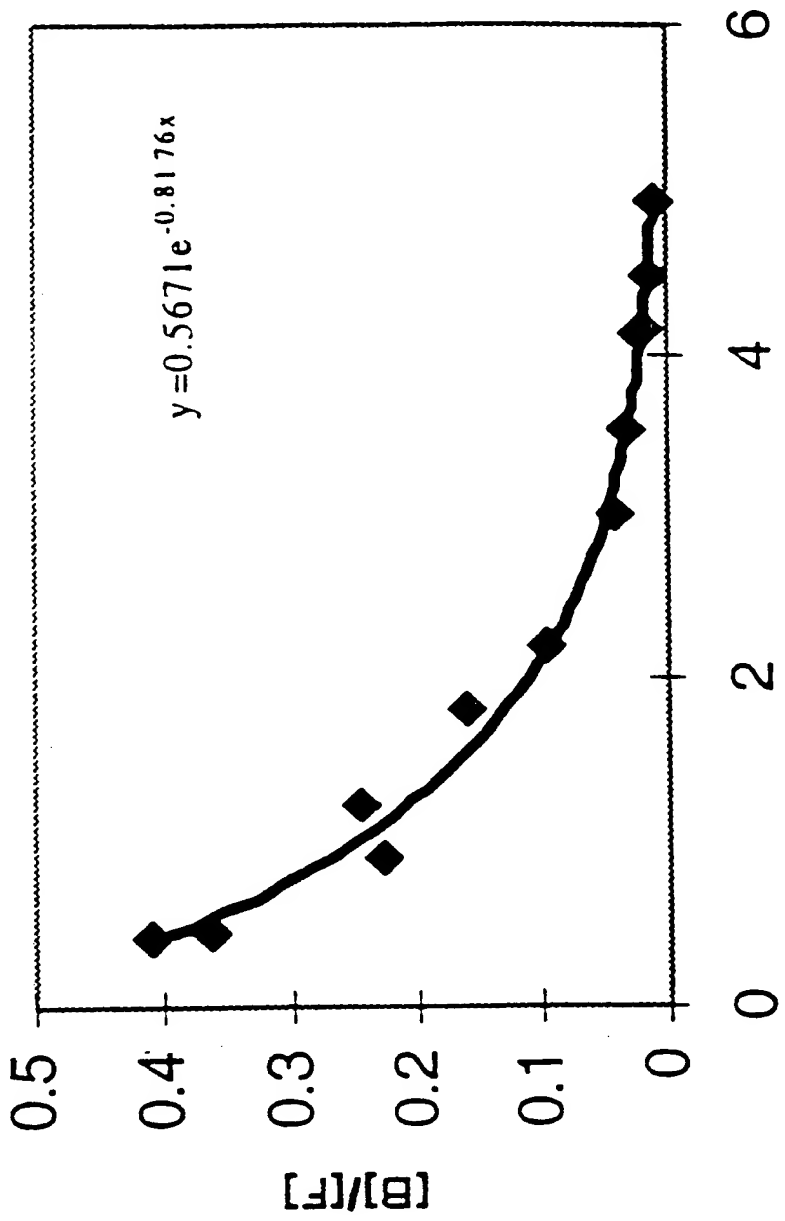
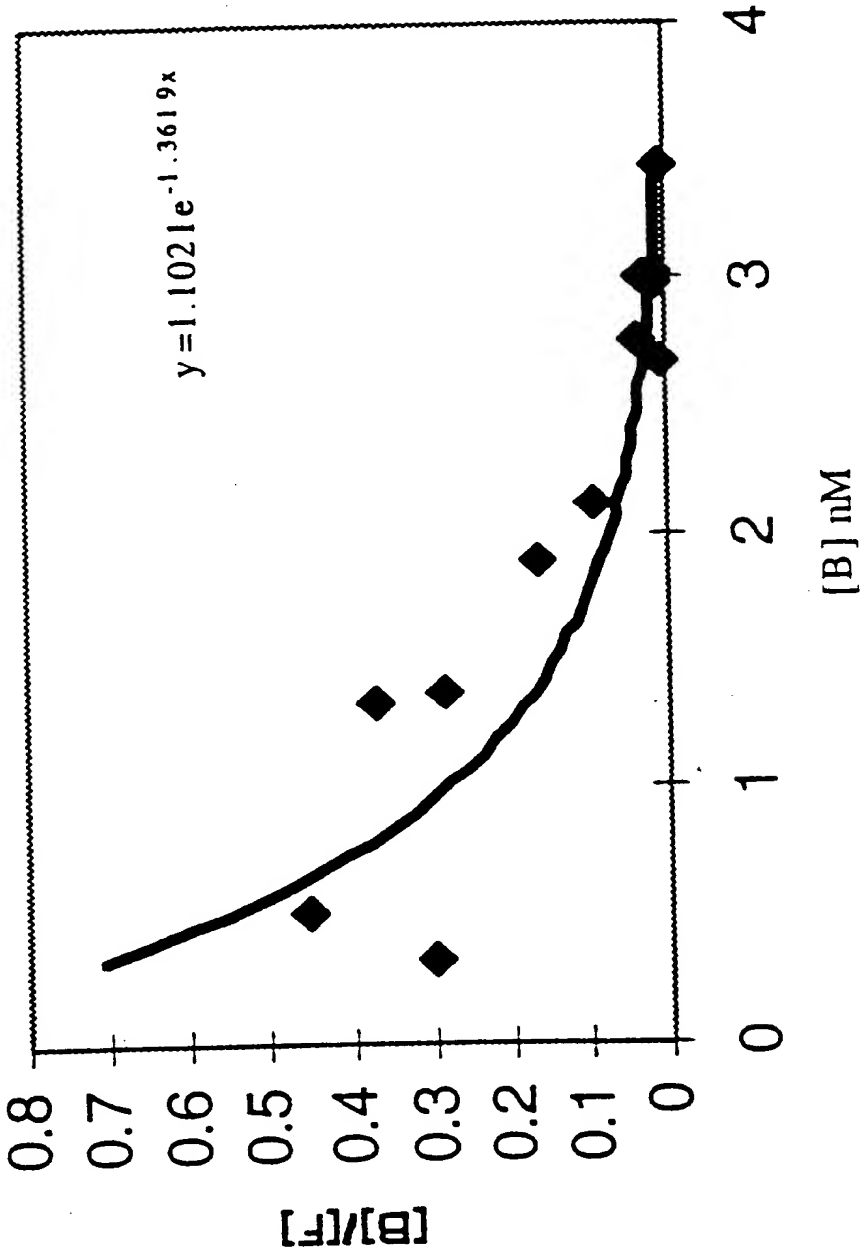

Scatchard (without 5-HT)
y=0.5671e^-0.8176x
[B]/[F]
0.5
0.4
0.3
0.2
0.1
0
0
2
4
6
[B] nM.

FIG. 17

FIG. 17(contd.)

Scatchard (+2.38mM 5-HT)



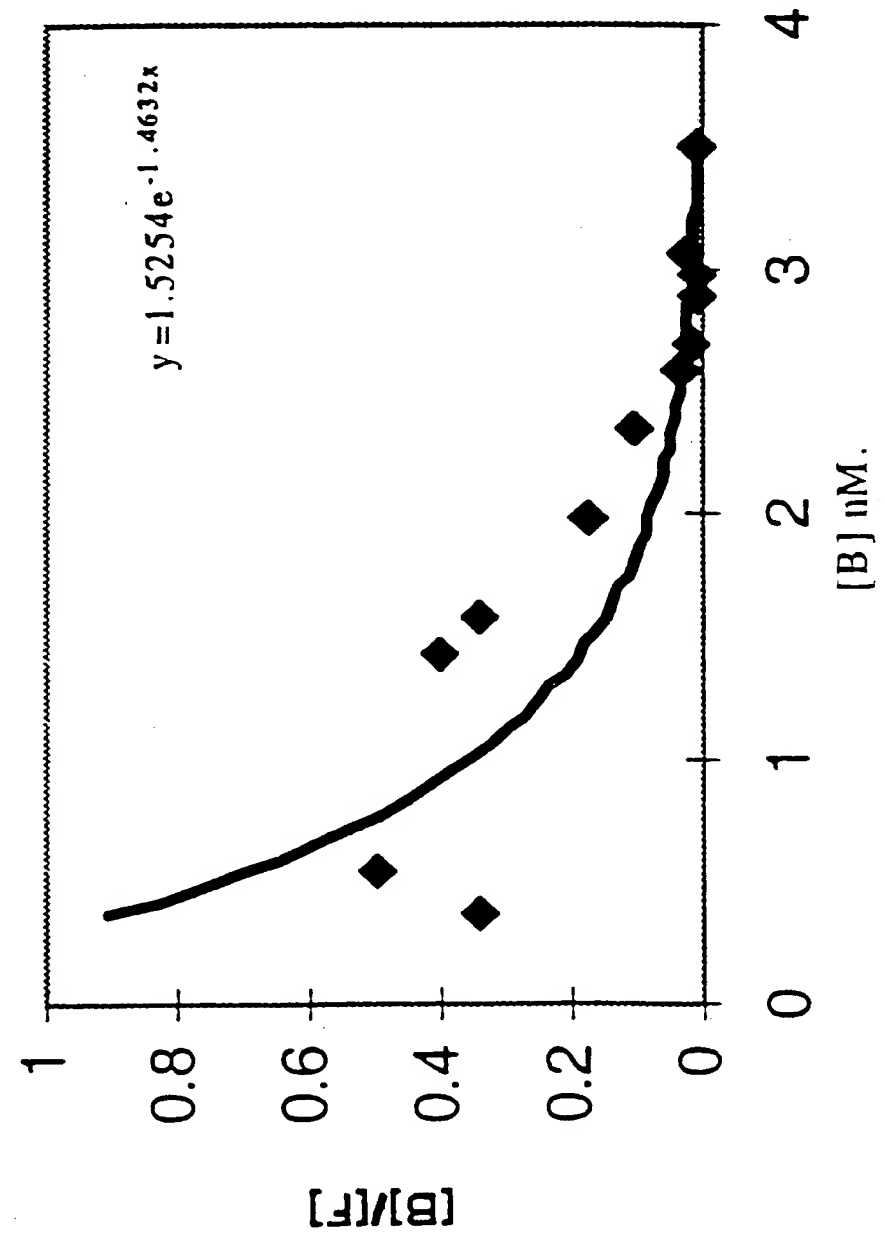

Scatchard (+23.8nM 5-HT)
y=1.5254e-1.4632x
[B]/[F]
[B] nM.
0
0.2
0.4
0.6
0.8
1
0
1
2
3
4

FIG. 17(contd.)

FIG. 18

FIG. 19

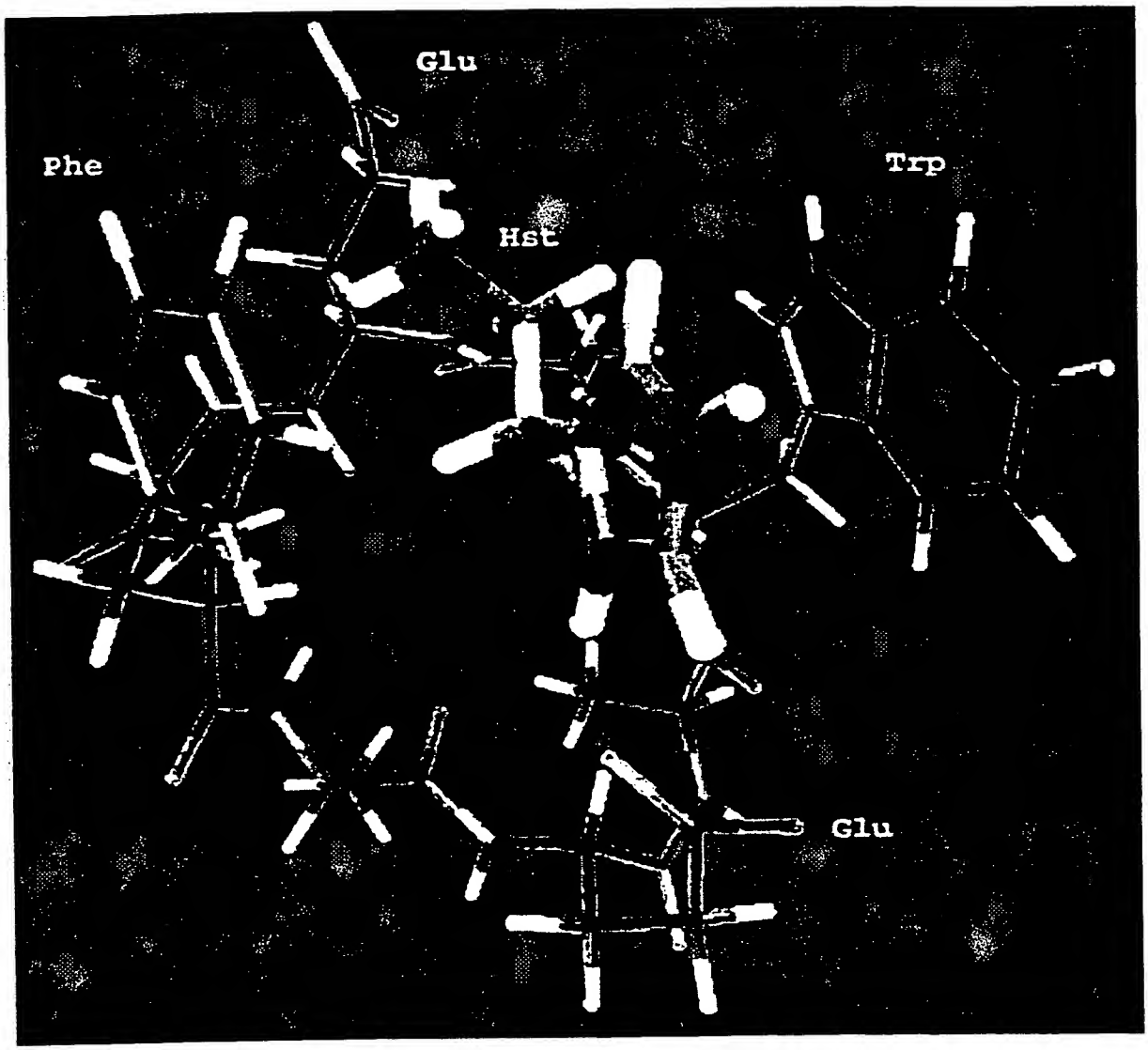


FIG. 20(a)

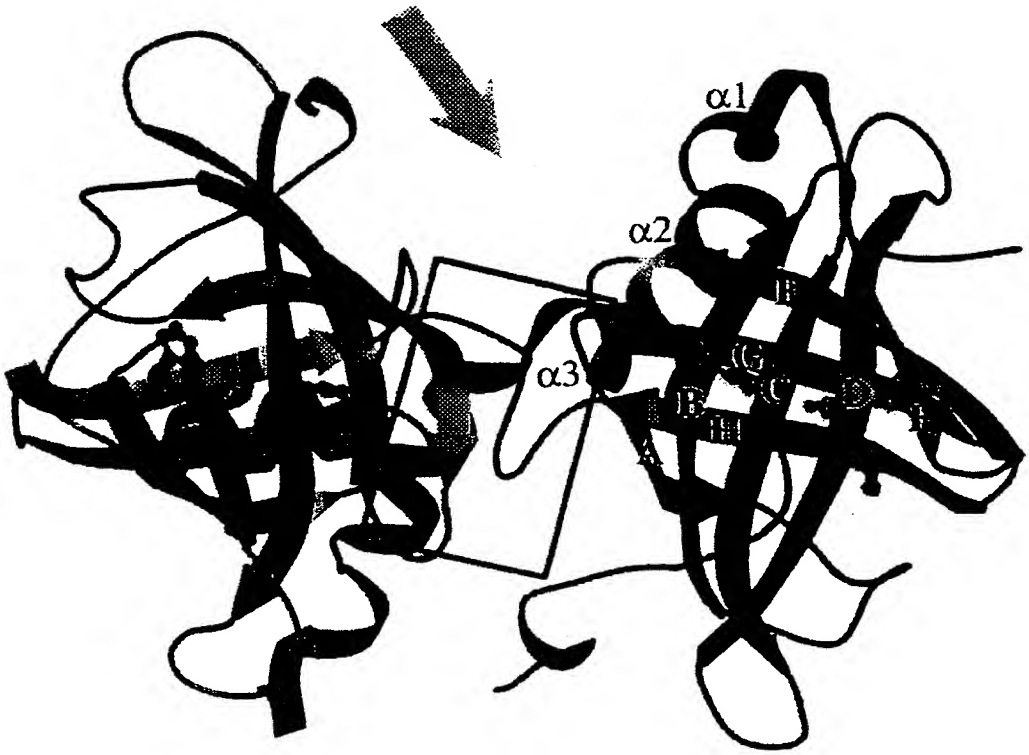


FIG. 20(b)

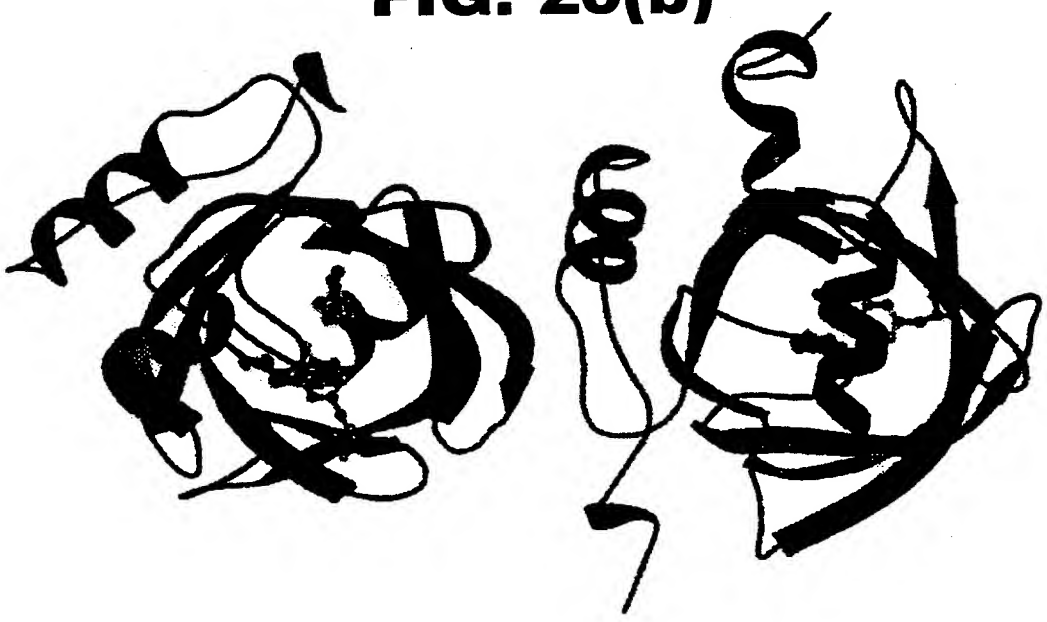


FIG. 20(c)

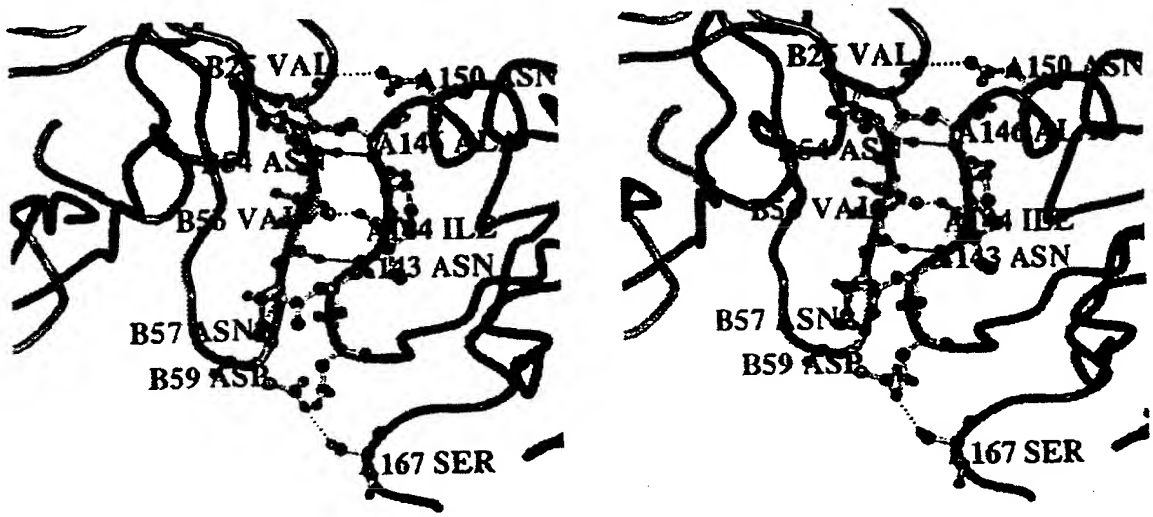


FIG. 20(d)

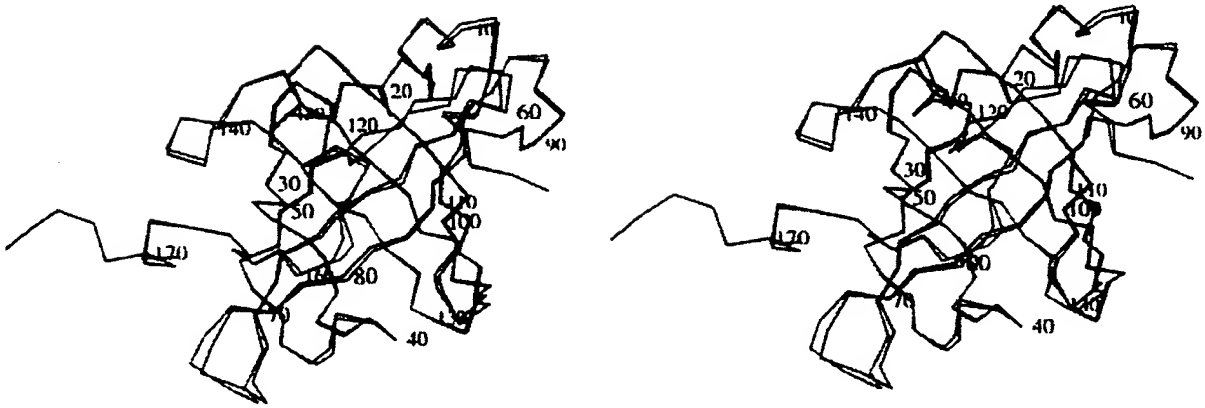


FIG. 21(a)

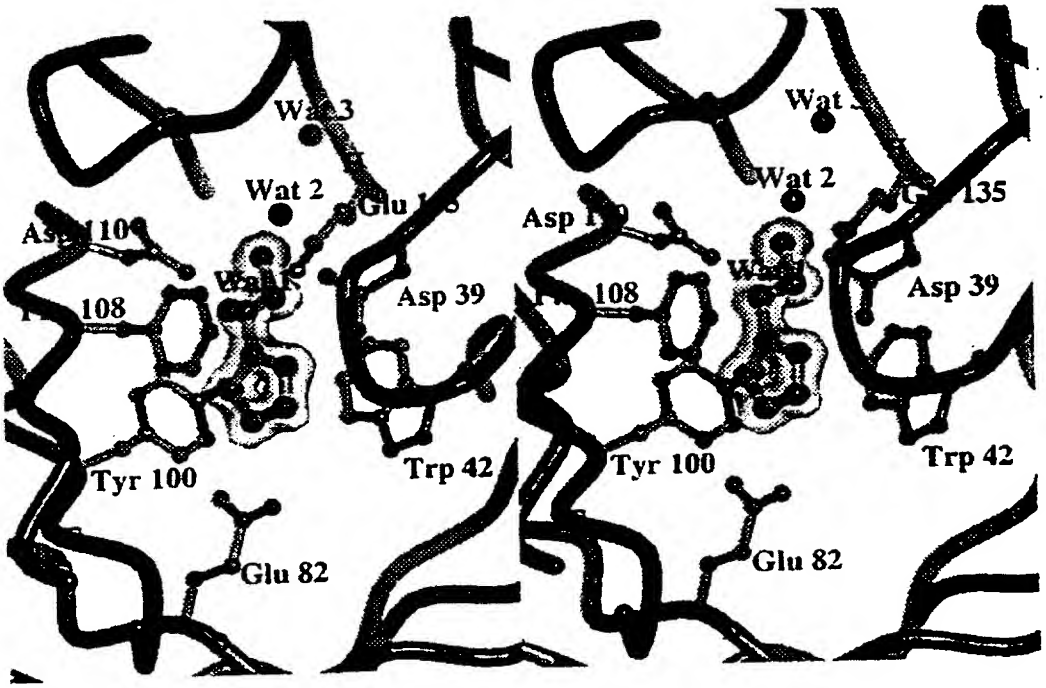


FIG. 21(b)

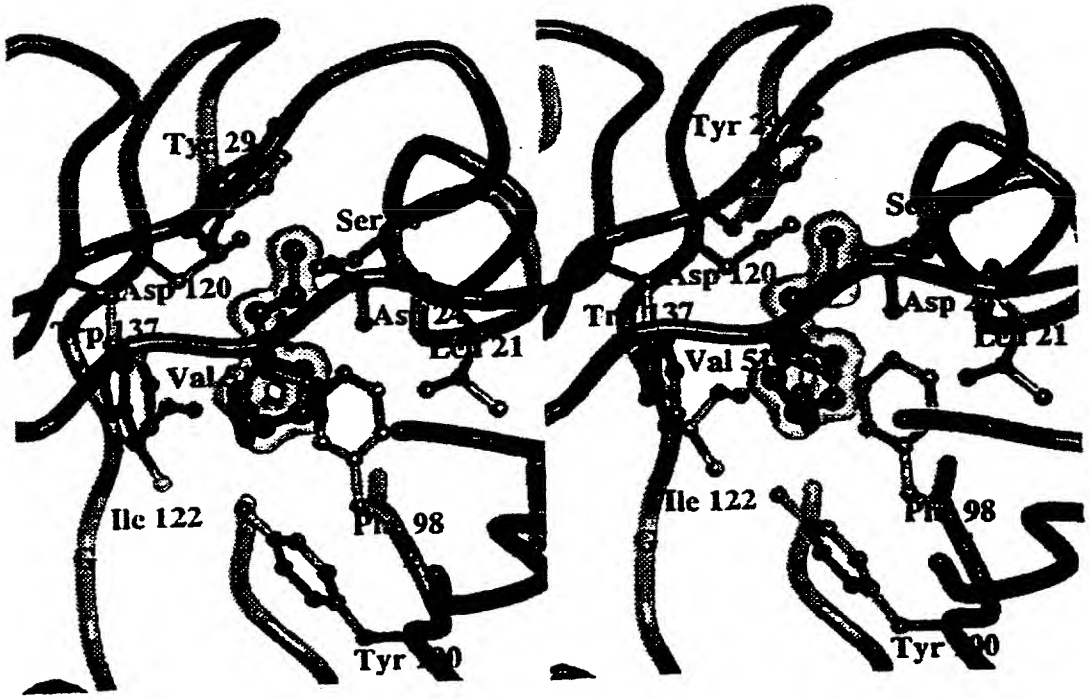


FIG. 21(c)


Tyr 29
Wat 7
Ser
Asp 120
Wat
Asp
Wat 5
Leu 21
Val 51
Wat 4
Ile 122
Phe
Tyr 100
Tyr
Wat 7
Ser
Asp 120
Wat 5
Val 51
Wat 4
Ile 122
Phe
Tyr 100

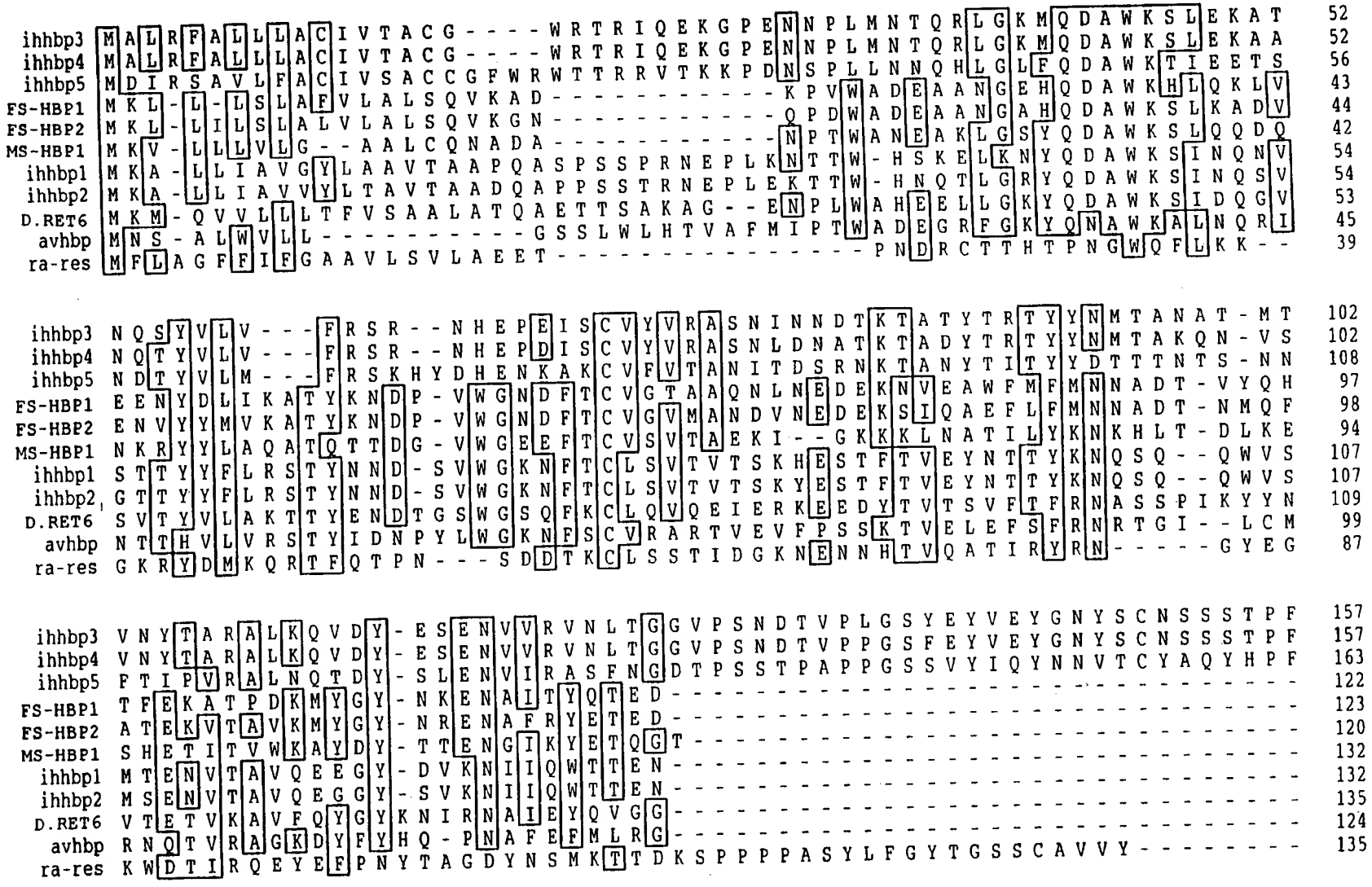

ihhbp3 MALRFALLLACCIVTACG----WRTRIQEKGPENNPLMNTQRLGKMQDAWKSLEKAT 52
ihhbp4 MALRFALLLACCIVTACG----WRTRIQEKGPENNPLMNTQRLGKMQDAWKSLEKAA 52
ihhbp5 MDIRSAVLFACCIVSACCGFWRWTTRRVTKKPDNSPLLNNQHLGLFQDAWKTIEETS 56
FS-HBP1 MKL-L-LSLAFVLALSQVKAD----------KPVWADEAANGEHQDAWKHLQKLV 43
FS-HBP2 MKL-LILSLALVLALSQVKGN----------QPDWADEAANGAHQDAWKSLKADV 44
MS-HBP1 MKV-LLLVLG--AALCQNADA----------NPTW-ANEAKLGSYQDAWKSLQQDQ 42
ihhbp1 MKA-LLIAVGYLAAVTAAPQASPSSPRNEPLKNTTW-HSKELKNYQDAWKSINQNV 54
ihhbp2 MKA-LLIAVVYLTAVTAADQAPPSSTRNEPLEKTTW-HNQTLGRYQDAWKSINQSV 54
D.RET6 MKM-QVVLLLTFVSAALATQAETTSAKAG--ENPLWAHEELLGKYQDAWKSIDQGV 53
avhbp MNS-ALWVLL----------GSSLWLHTVAFMIPTWADEGRFGKYQNAWKALNQRI 45
ra-res MFLAGFFIFGAAVLSVLAEET----------PNDRCTTHTPNGWQFLKK-- 45
ihhbp3 NQSYVLV---FRSR--NHEPEISCVYVRASNINNDTKTATYTRTYYNMTANAT-MT 102
ihhbp4 NQTYVLV---FRSR--NHEPDISCVYVRASNLDNATKTADYTRTYYNMTAKQN-VS 102
ihhbp5 NDTYVLM---FRSKHYDHENKAKCVFVTAANITDSRNKTANYTITYYDTTTNTS-NN 108
FS-HBP1 EENYDLIKATYKNDP-VWGNDFTCVGTAAQNLNEDEKNVEAWFMFMNNADT-VYQH 97
FS-HBP2 ENVYYMVKATYKNDP-VWGNDFTCVGVMAANDVNEDEKSIQAEFLFMNNADT-NMQF 98
MS-HBP1 NKRYYLAQATQTTDG-VWGEEFTCVSVTAEKI--GKKKLNATILYKNKHLT-DLKE 94
ihhbp1 STTYYFLRSTYNND-SVWGKNFTCLSVTVTSKHESTFTVEYNTTYKNQSQ--QWVS 107
ihhbp2 GTTYYFLRSTYNND-SVWGKNFTCLSVTVTSKYESTFTVEYNTTYKNQSQ--QWVS 107
D.RET6 SVTYVLAKTTYENDTGSWGSQFKCLQVQEIERKEEDYTVTSVFTFRNASSPIKYYN 109
avhbp NTTHVLVRSTYIDNPYLWGKNFSCVRARTVEVFPSSKTVELEFSFRNRTGI--LCM 99
ra-res GKRYDMKQRTFQTPN---SDDTKCLSSTIDGKNENNHTVQATIRYRN------GYEG 87
ihhbp3 VNYTARALKQVDY-ESENVVRVNLTGGVPSNDTVPLGSYEYVEYGNYSCNSSSTPF 157
ihhbp4 VNYTARALKQVDY-ESENVVRVNLTGGVPSNDTVPPGSFEYVEYGNYSCNSSSTPF 157
ihhbp5 FTIPVRALNQTDY-SLENVIRASFNGDTPSSTPAPPGSSVYIQYNNVTCYAQYHPF 163
FS-HBP1 TFEKATPDKMYGY-NKENAITYQTED---------- 122
FS-HBP2 ATEKVTAVKMYGY-NRENAFRYETED---------- 123
MS-HBP1 SHETITVWKAYDY-TTENGIKYETQGT---------- 120
ihhbp1 MTENVTAVQEEGY-DVKNIIQWTTEN---------- 132
ihhbp2 MSENVTAAVQEGGY-SVKNIIQWTTEN---------- 132
D.RET6 VTETVKAAVFQYGYKNIRNAIEYQVGG---------- 135
avhbp RNQTVRAGKDYFYHQ-PNAFEFMLRG---------- 124
ra-res KWDTIRQEYEFPNYTAGDYNSMKTTDKSPPPPASYLFGYTGSSCAVVY---------- 135

FIG. 22


ihhbp3 L D A V - - - - - - Q M A S Q G Q S R G P D I E G R T Y L D F Y V V Y N Q P S C N V L - - - - K S P L L G G A C 203
ihhbp4 L D A V - - - - - - Q M A S Q G Q S W G P D V E G R T Y L D F Y V V Y N Q P S C N V L - - - - K S P L L G G A C 203
ihhbp5 S N N G I S A K Y D E M P R D G R N Y L F D N F I G A Y L D F Y V V F S Q P T C N V L - - - - R - - - V R E G C 212
FS-HBP1 - G Q V L T D V L A F S D - D N C Y V I Y A L G P D G S G A G - Y 152
FS-HBP2 - G Q V F T D V I A Y S D - D N C D V I Y V P G T D G N E E G - Y 153
MS-HBP1 - R T Q T F E D V F V F S D Y K N C D V I F V P K E R G S D E G D Y 153
ihhbp1 - N T K F N D T V V F T D G Q T C D L L Y I P Y K E N - - G - - Y 160
ihhbp2 - N T K F N D T V V F T D G Q T C D V L Y I P Y K E D - - G - - Y 160
D.RET6 - G L N I T D T L I F T D G E L C D V F Y V P N A D Q - - G - - C 163
avhbp - N R S F S N A V M F T D G M T C N L L S F P Y Q R N K P Q - - C 154
ra-res - V N S I G P V R S N S E N P P E R L T A S Q E S A Q R D C 164
ihhbp3 D F W V T E S E L Q K A L - N K T S E K K K T K L E A R A R K A G - - - - - - 235
ihhbp4 D F W V P Q S E L D K V L - N K K G D K K K P A - K S S S Q N G D - - - - - - 234
ihhbp5 D F W L R K T E L P S L L K A A E N D D N D N T E S L K N Y W E R R I N N T K T R F R H N T K K C K M Y V Q R Y 268
FS-HBP1 E L W A T D - 158
FS-HBP2 E L W T T D - 159
MS-HBP1 E L W V S E D K - 161
ihhbp1 E L W V R S D Y - 168
ihhbp2 E L W V R S E Y - 168
D.RET6 E L W V K K S H - 171
avhbp E L W V K D T R - 162
ra-res V L W V D H D E K A T Q - 176
ihhbp3 G D S D D Q G P E L E V V F K N L P P P C R A A F I T S C G Y P T F L M Y N K T I C N - - - R T D S A A V 285
ihhbp4 E G S D A E Q P E L E A I F K H L P P P C R A A F I T S C G Y P N F L M Y N K T I C N - - - A A G H A A N 284
ihhbp5 S I E K A E D V F K N T A F K H L P S D C R F A F L A A C G N P A F T I Y D P E T C N S S L P A N M A E S 321
FS-HBP1 - - - - - - - - - - - - - Y T D V P A S C L E K F N E Y A A G L P - - V R D - V Y T - - - - - S D C L P E 190
FS-HBP2 - - - - - - - - - - - - - Y D N I P A N C L N K F N E Y A V G R E - - T R D - V F T - - - - - S A C L - E 190
MS-HBP1 - - - - - - - - - - - - - I D K I P D C C K F T M A Y F A Q Q Q E K T V R N - V Y T D S S C K P A P A Q N 200
ihhbp1 - - - - - - - - - - - - - L Q N T P T C C Q F I F D - L V A - L G R T T Y N - I S T P D C V T K T S R - - 203
ihhbp2 - - - - - - - - - - - - - L Q N T P T C C Q F I F D - L V A - L G R T T Y N - I S T P N C V A T T A G - - 203
D.RET6 - - - - - - - - - - - - - Y K H V P D Y C T F V F N V F C A - K D R K T Y D - I F N E E C V Y N G E P W L 209
avhbp - - - - - - - - - - - - - V D N I P P C C S F M F D Y L C P - Q P R P F - - - I I Y D K A M C T V R P P R 198
ra-res - - - - - - - - - - - - - - - - - E Q C C E D F F K T H C K E T V H V I Y D V N R C - - - - - K E N G S E 207

FIG. 22(CONTD.)